

Appl. No. 09/918,421

R E M A R K S

Examiners Clow and Moran are thanked for having a telephone interview with the undersigned on February 9, 2006. Claims 6, 9, 10 and 12 were discussed during the telephone interview. The general thrust of the position of the Examiners, as expressed to the undersigned during the telephone interview, was that there was terminology in the aforesaid claims, especially claim 6, that was unclear. The Examiners said that if applicants wished to obtain entry of an amendment to the claims, such amendment should be filed within a few weeks of the interview.

During a telephone interview on February 21, 2006 between Examiner Moran and the undersigned, the undersigned asked Examiner Moran the latest date for filing this AMENDMENT to have the best chance of entry of the AMENDMENT. Examiner Moran said that the AMENDMENT should be filed no later than February 27, 2006.

The terms "probe" and "primer" are recited in the preamble of claim 6. The term "probe" is supported on page 9, lines 19 and 24 and on page 10 of the specification. The term "primer" is also supported on page 10 of the specification.

Appl. No. 09/918,421

Steps (a1) and (a3) of amended claim 6 contain features supported in the specification on page 12, line 19 to page 14, line 11.

Step (c) in claim 6 now clearly recites the extraction of all candidate nucleotide sequences which are present on the nucleotide sequences of the target nucleic acid. As illustrated in Fig. 3 and described in the specification on page 14, lines 12 to 22, the extraction step represents a listing of all possible candidate nucleotide sequences by way of simple mathematical procedures.

Following the suggestion of the Examiners during the aforesaid telephone interview on February 9, 2006, the previous recitations in claim 6 of "listing" was changed to the terminology of "extracting," as originally recited in claim 6.

In step (d) of claim 6, the method of extracting "all of the n unit sequences contained in each of the candidate sequences" is a mathematical procedure as in the case of the method of

Appl. No. 09/918,421

extracting all n unit sequences contained in the genome in step (a2) of claim 6.

Step (e) of claim 6 recites the procedure of calculating an occurrence frequency index. Further, step (e) clearly describes that all occurrence frequencies of all the n unit sequences are multiplied with each other.

Claim (g1) of claim 6 recites a feature of previous claim 9, namely "stability of an intramolecular structure." Step (g1) is supported in the specification on page 17, lines 15 to 18. The stability of the intramolecular secondary structure can be calculated from the possibility of causing intramolecular hybridization within the nucleotide sequence and the thermal stability of the base pairs created thereby.

Step (g2) of claim 6 recites the procedure for selecting the "most promising candidate."

New claim 13 recites features of amended claim 6 and previous claim 9 ("Tm"). Steps (g1) and (g2) of claim 13 are supported on page 16, lines 12 to 16 and page 17, lines 15 to 18 of the specification. In step (g1) of claim 13, the Tm of a nucleotide sequence can be calculated from the thermal stability

Appl. No. 09/918,421

of all base pairs contained in double strand form, formed by hybridization with its complimentary chain (see page 16, lines 8 to 12 of the specification).

New claim 14 recites the features of claim 11.


New claim 15 recites the features of amended claim 12.

Reconsideration is requested. Allowance is solicited.

If the Examiner has any comments, questions, objections or recommendations, the Examiner is invited to telephone the undersigned at the telephone number given below for prompt action.

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